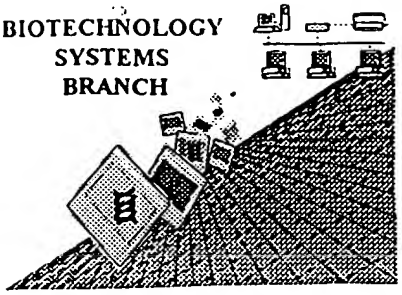
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

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TECH CENTER 1600/2900

Application Serial Number: 09/455,978

Source: OIPE

Date Processed by STIC: 7/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 09/455,978

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)___ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 07/07/2001
PATENT APPLICATION: US/09/455,978 TIME: 13:15:00

Input Set : A:\H1020011.app
Output Set: N:\CRF3\07062001\I455978.raw

<110> APPLICANT: Alam, Maqsudul
Larsen, Randy
<120> TITLE OF INVENTION: HEME PROTEINS HEMAT-HS AND HEMAT-BS AND THEIR USE IN MEDICINE AND MICROSENSORS
<130> FILE REFERENCE: 201040/1020
<140> CURRENT APPLICATION NUMBER: 09/455,978
<141> CURRENT FILING DATE: 1999-12-06
<160> NUMBER OF SEQ ID NOS: 86
<170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed
see page 5

<210> SEQ ID NO: 1
<211> LENGTH: 1470
<212> TYPE: DNA
<213> ORGANISM: Halobacterium salinarum
<400> SEQUENCE: 1

atgagcaacg ataatgacac tctcgtgacc gccgacgttc ggaacgggat cgacgggcac 60
gcactcgcgg accggatcgg cctcgacgag gcggagatcg cgtggcggct gtcgttcacc 120
gggatcgacg acgacacgat ggccgcgctc gccgccgaac agccgctgtt cgaagccacc 180
gcggacgcgc tggtgaccga cttctacgac cacttggagt cctacgagcg cacacaggac 240
ctcttcgcga actccacgaa gaccgtcgag caactcaaag agacgcaggc cgagtacttg 300
ctgggcctcg ggcgcggcga gtacgacacc gagtacgccg cccagcgcgc ccgtatcggg 360
aagatacacg acgtgctcgg gctcggaccg gacgtctatc tgggcgcgta cacgcgatac 420
tacacggggc tgttggacgc gcttgccgac gacgtggtcg ccgaccgcgg cgaggaggcg 480
gccgccgccg tcgacgaact cgtggcccgg ttcctgccga tgttgaagct gttgaccttc 540
gatcagcaga tcgcaatgga cacctacatc gactcgtacg cccagcgcct ccacgacgag 600
atcgacagcc gccaggagtt ggcgaacgcg gtcgccacgc acgtggaagc accgctgtcc 660
tcgctggagg cgacctcgca ggacgtcgcc gagcgcacgg acacgatgcg ggcccgcacc 720
gacgaccagg tcgaccgcat ggctgacgtc agccgtgaga tatccagcgt gtccgcgagc 780
gtcgaggagg tcgcctcgac ggccgacgac gtccgccgga ccagcgagga cgccgaggcg 840
ctggcccagc agggcgaggc ggccgccgac gacgcgctcg ccacgatgac cgacatcgac 900
gaggcgaccg acggcgtcac cgcgggcgtc gaacagctcg gcgagcgcgc cgccgacgtc 960
gaatcagtga ccggcgtgat cgacgacatc gccgagcaga cgaacatgct ggcgctgaac 1020
gcgtccatcg aggccgcccg cgccggggag gcgggcgagg ggtttgcggt cgtcgccgac 1080
gaggtcaagg ccctcgccga ggagtcccgc gagcagtcca cgcgcgtcga ggagctcgtc 1140
gagcagatgc aggcggagac cgaggagacg gtcgaccagt tggacgaggt caaccagcgc 1200
atcggcgagg gcgtcgagcg cgtcgaggag gcgatggaga ccctccagga gatcaccgac 1260
gccgtcgagg acgccgcaag cgggatgcag gaggtgtcga cggcgaccga cgaacaggcg 1320
gtgagcaccg aggaggtcgc cgagatggtc gacggtgtcg acgaccgcgc gggcgagatc 1380
gcggccgccc tcgatgacat cgccgacgcg accgatcagc aggtccggac cgtcgaggag 1440
gtccgcgaga cggtcggcaa gctcagctag 1470

<210> SEQ ID NO: 2
<211> LENGTH: 489
<212> TYPE: PRT
<213> ORGANISM: Halobacterium salinarum
<400> SEQUENCE: 2

Met Ser Asn Asp Asn Asp Thr Leu Val Thr Ala Asp Val Arg Asn Gly
1 5 10 15
Ile Asp Gly His Ala Leu Ala Asp Arg Ile Gly Leu Asp Glu Ala Glu

RAW SEQUENCE LISTING DATE: 07/07/2001
PATENT APPLICATION: US/09/455,978 TIME: 13:15:00

Input Set : A:\H1020011.app
Output Set: N:\CRF3\07062001\I455978.raw

```
61                20                  25                  30
63 Ile Ala Trp Arg Leu Ser Phe Thr Gly Ile Asp Asp Asp Thr Met Ala
64           35                  40                  45
66 Ala Leu Ala Ala Glu Gln Pro Leu Phe Glu Ala Thr Ala Asp Ala Leu
67       50                  55                  60
69 Val Thr Asp Phe Tyr Asp His Leu Glu Ser Tyr Glu Arg Thr Gln Asp
70   65                  70                  75                  80
72 Leu Phe Ala Asn Ser Thr Lys Thr Val Glu Gln Leu Lys Glu Thr Gln
73                   85                  90                  95
75 Ala Glu Tyr Leu Leu Gly Leu Gly Arg Gly Glu Tyr Asp Thr Glu Tyr
76               100                 105                 110
78 Ala Ala Gln Arg Ala Arg Ile Gly Lys Ile His Asp Val Leu Gly Leu
79           115                 120                 125
81 Gly Pro Asp Val Tyr Leu Gly Ala Tyr Thr Arg Tyr Tyr Thr Gly Leu
82       130                 135                 140
84 Leu Asp Ala Leu Ala Asp Asp Val Val Ala Asp Arg Gly Glu Glu Ala
85 145                 150                 155                 160
87 Ala Ala Ala Val Asp Glu Leu Val Ala Arg Phe Leu Pro Met Leu Lys
88                   165                 170                 175
90 Leu Leu Thr Phe Asp Gln Gln Ile Ala Met Asp Thr Tyr Ile Asp Ser
91               180                 185                 190
93 Tyr Ala Gln Arg Leu His Asp Glu Ile Asp Ser Arg Gln Glu Leu Ala
94           195                 200                 205
96 Asn Ala Val Ala Thr His Val Glu Ala Pro Leu Ser Ser Leu Glu Ala
97       210                 215                 220
99 Thr Ser Gln Asp Val Ala Glu Arg Thr Asp Thr Met Arg Ala Arg Thr
100 225                 230                 235                 240
102 Asp Asp Gln Val Asp Arg Met Ala Asp Val Ser Arg Glu Ile Ser Ser
103                  245                 250                 255
105 Val Ser Ala Ser Val Glu Glu Val Ala Ser Thr Ala Asp Asp Val Arg
106              260                 265                 270
108 Arg Thr Ser Glu Asp Ala Glu Ala Leu Ala Gln Gln Gly Glu Ala Ala
109          275                 280                 285
111 Ala Asp Asp Ala Leu Ala Thr Met Thr Asp Ile Asp Glu Ala Thr Asp
112      290                 295                 300
114 Gly Val Thr Ala Gly Val Glu Gln Leu Gly Glu Arg Ala Ala Asp Val
115 305                 310                 315                 320
117 Glu Ser Val Thr Gly Val Ile Asp Asp Ile Ala Glu Gln Thr Asn Met
118                  325                 330                 335
120 Leu Ala Leu Asn Ala Ser Ile Glu Ala Ala Arg Ala Gly Glu Ala Gly
121              340                 345                 350
123 Glu Gly Phe Ala Val Val Ala Asp Glu Val Lys Ala Leu Ala Glu Glu
124          355                 360                 365
126 Ser Arg Glu Gln Ser Thr Arg Val Glu Glu Leu Val Glu Gln Met Gln
127      370                 375                 380
129 Ala Glu Thr Glu Glu Thr Val Asp Gln Leu Asp Glu Val Asn Gln Arg
130 385                 390                 395                 400
132 Ile Gly Glu Gly Val Glu Arg Val Glu Glu Ala Met Glu Thr Leu Gln
133                  405                 410                 415
```

RAW SEQUENCE LISTING DATE: 07/07/2001
PATENT APPLICATION: US/09/455,978 TIME: 13:15:00

Input Set : A:\H1020011.app
Output Set: N:\CRF3\07062001\I455978.raw

```
135 Glu Ile Thr Asp Ala Val Glu Asp Ala Ala Ser Gly Met Gln Glu Val
136             420                 425                 430
138 Ser Thr Ala Thr Asp Glu Gln Ala Val Ser Thr Glu Glu Val Ala Glu
139         435                 440                 445
141 Met Val Asp Gly Val Asp Asp Arg Ala Gly Glu Ile Ala Ala Ala Leu
142     450                 455                 460
144 Asp Asp Ile Ala Asp Ala Thr Asp Gln Gln Val Arg Thr Val Glu Glu
145 465                 470                 475                 480
147 Val Arg Glu Thr Val Gly Lys Leu Ser
148                 485
151 <210> SEQ ID NO: 3
152 <211> LENGTH: 1390
153 <212> TYPE: DNA
154 <213> ORGANISM: Bacillus subtilis
156 <400> SEQUENCE: 3
157 atgttattta aaaaagacag aaaacaagaa acagcttact tttcagattc aaacggacaa 60
158 caaaaaaacc gcattcagct cacaaacaaa catgcagatg tcaaaaaaca gctcaaaatg 120
159 gtcaggttgg gagatgctga gctttatgtg ttagagcagc ttcagccact cattcaagaa 180
160 aatatcgtaa atatcgtcga tgcgttttat aaaaaccttg accatgaaag ctcattgatg 240
161 gatatcatta atgatcacag ctcagttgac cgcttaaaac aaacgttaaa acggcatatt 300
162 caggaaatgt ttgcaggcgt tatcgatgat gaatttattg aaaagcgtaa ccgaatcgcc 360
163 tccatccatt taagaatcgg ccttttgcca aaatggtata tgggtgcgtt tcaagagctc 420
164 cttttgtcaa tgattgacat ttatgaagcg tccattacaa atcagcaaga actgctaaaa 480
165 gccattaaag caacaacaaa aatcttgaac ttagaacagc agcttgtcct tgaagcgttt 540
166 caaagcgagt acaaccagac ccgtgatgaa caagaagaaa agaaaaacct tcttcatcag 600
167 aaaattcaag aaacctctgg atcgattgcc attctgtttt cagaaacaag cagatcagtt 660
168 caagagcttg tggacaaatc tgaaggcatt tctcaagcat ccaaagccgg cactgtaaca 720
169 tccagcactg ttgaagaaaa gtcgatcggc ggaaaaaaag agctagaagt ccagcaaaaa 780
170 cagatgaaca aaattgacac aagccttgtc caaatcgaaa aagaaatggt caagctggat 840
171 gaaatcgcgc agcaaattga aaaaatcttc ggcatcgtca caggcatagc tgaacaaaca 900
172 aaccttctct cgctcaatgc atctattgaa tccgcccgcg ccggagaaca cggcaaaggc 960
173 tttgctgtcg tggcaaatga agtgcggaag ctttctgagg atacgaaaaa aaccgtctct 1020
174 actgtttctg agcttgtgaa caatacgaat acacaaatca acattgtatc caagcatatc 1080
175 aaagacgtga atgagctagt cagcgaaagt aaagaaaaaa tgacgcaaat taaccgctta 1140
176 ttcgatgaaa tcgtccacag catgaaaatc agcaaagagc aatcaggcaa aatcgacgtc 1200
177 gatctgcaag cctttcttgg agggcttcag gaagtcagcc gcgccgtttc ccatgtggcc 1260
178 gcttccgttg attcgcttgt catcctgaca gaagaataac catcaaaaac cggtctgcca 1320
179 tacggccggt ttttttgcgt tcattatgta aacttaaatt aaaaatcagt tgacataata 1380
180 attacctgca                                                       1390
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 432
185 <212> TYPE: PRT
186 <213> ORGANISM: Bacillus subtilis
188 <400> SEQUENCE: 4
189 Met Leu Phe Lys Lys Asp Arg Lys Gln Glu Thr Ala Tyr Phe Ser Asp
190   1               5                  10                  15
192 Ser Asn Gly Gln Gln Lys Asn Arg Ile Gln Leu Thr Asn Lys His Ala
193             20                  25                  30
195 Asp Val Lys Lys Gln Leu Lys Met Val Arg Leu Gly Asp Ala Glu Leu
```

RAW SEQUENCE LISTING DATE: 07/07/2001
PATENT APPLICATION: US/09/455,978 TIME: 13:15:00

Input Set : A:\H1020011.app
Output Set: N:\CRF3\07062001\I455978.raw

```
196          35                  40                  45
198 Tyr Val Leu Glu Gln Leu Gln Pro Leu Ile Gln Glu Asn Ile Val Asn
199      50                  55                  60
201 Ile Val Asp Ala Phe Tyr Lys Asn Leu Asp His Glu Ser Ser Leu Met
202  65                  70                  75                  80
204 Asp Ile Ile Asn Asp His Ser Ser Val Asp Arg Leu Lys Gln Thr Leu
205                  85                  90                  95
207 Lys Arg His Ile Gln Glu Met Phe Ala Gly Val Ile Asp Asp Glu Phe
208              100                 105                 110
210 Ile Glu Lys Arg Asn Arg Ile Ala Ser Ile His Leu Arg Ile Gly Leu
211          115                 120                 125
213 Leu Pro Lys Trp Tyr Met Gly Ala Phe Gln Glu Leu Leu Leu Ser Met
214      130                 135                 140
216 Ile Asp Ile Tyr Glu Ala Ser Ile Thr Asn Gln Gln Glu Leu Leu Lys
217 145                 150                 155                 160
219 Ala Ile Lys Ala Thr Thr Lys Ile Leu Asn Leu Glu Gln Gln Leu Val
220                 165                 170                 175
222 Leu Glu Ala Phe Gln Ser Glu Tyr Asn Gln Thr Arg Asp Glu Gln Glu
223              180                 185                 190
225 Glu Lys Lys Asn Leu Leu His Gln Lys Ile Gln Glu Thr Ser Gly Ser
226          195                 200                 205
228 Ile Ala Asn Leu Phe Ser Glu Thr Ser Arg Ser Val Gln Glu Leu Val
229      210                 215                 220
231 Asp Lys Ser Glu Gly Ile Ser Gln Ala Ser Lys Ala Gly Thr Val Thr
232 225                 230                 235                 240
234 Ser Ser Thr Val Glu Glu Lys Ser Ile Gly Gly Lys Lys Glu Leu Glu
235                 245                 250                 255
237 Val Gln Gln Lys Gln Met Asn Lys Ile Asp Thr Ser Leu Val Gln Ile
238              260                 265                 270
240 Glu Lys Glu Met Val Lys Leu Asp Glu Ile Ala Gln Gln Ile Glu Lys
241          275                 280                 285
243 Ile Phe Gly Ile Val Thr Gly Ile Ala Glu Gln Thr Asn Leu Leu Ser
244      290                 295                 300
246 Leu Asn Ala Ser Ile Glu Ser Ala Arg Ala Gly Glu His Gly Lys Gly
247 305                 310                 315                 320
249 Phe Ala Val Val Ala Asn Glu Val Arg Lys Leu Ser Glu Asp Thr Lys
250                 325                 330                 335
252 Lys Thr Val Ser Thr Val Ser Glu Leu Val Asn Asn Thr Asn Thr Gln
253              340                 345                 350
255 Ile Asn Ile Val Ser Lys His Ile Lys Asp Val Asn Glu Leu Val Ser
256          355                 360                 365
258 Glu Ser Lys Glu Lys Met Thr Gln Ile Asn Arg Leu Phe Asp Glu Ile
259      370                 375                 380
261 Val His Ser Met Lys Ile Ser Lys Glu Gln Ser Gly Lys Ile Asp Val
262 385                 390                 395                 400
264 Asp Leu Gln Ala Phe Leu Gly Gly Leu Gln Glu Val Ser Arg Ala Val
265                 405                 410                 415
267 Ser His Val Ala Ala Ser Val Asp Ser Leu Val Ile Leu Thr Glu Glu
268              420                 425                 430
```

RAW SEQUENCE LISTING DATE: 07/07/2001
PATENT APPLICATION: US/09/455,978 TIME: 13:15:00

Input Set : A:\H1020011.app
Output Set: N:\CRF3\07062001\I455978.raw

```
     274 <210> SEQ ID NO: 5
     275 <211> LENGTH: 57
     276 <212> TYPE: PRT
     277 <213> ORGANISM: Artificial Sequence
     279 <220> FEATURE:
     280 <223> OTHER INFORMATION: Description of Artificial Sequence: Template
     281       sequence
     283 <220> FEATURE:
     284 <221> NAME/KEY: UNSURE
     285 <222> LOCATION: (4)
     286 <223> OTHER INFORMATION: X at any position in this sequence is unknown.
     288 <400> SEQUENCE: 5
W--> 289 Ile Ile Lys Xaa Thr Val Pro Val Leu Xaa Glu His Gly Xaa Xaa Ile
     290   1               5                  10                  15
W--> 292 Gly Gln Asp Val Leu Val Val Leu Ile Lys Xaa Asn Pro Glu Ile Gln
     293               20                  25                  30
W--> 295 Glu Lys Phe Phe Phe Phe Lys His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     296           35                  40                  45
W--> 298 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     299       50                  55
     302 <210> SEQ ID NO: 6
     303 <211> LENGTH: 55
     304 <212> TYPE: PRT
     305 <213> ORGANISM: Erwinia chrysanthemi
     307 <400> SEQUENCE: 6
     308 Ile Lys Ser Thr Ile Pro Leu Leu Ala Glu Thr Gly Pro Ala Leu Thr
     309   1               5                  10                  15
     311 Ala His Phe Tyr Gln Arg Met Phe His His Asn Pro Glu Leu Lys Asp
     312               20                  25                  30
     314 Ile Phe Asn Met Ser Asn Gln Arg Asn Gly Asp Gln Arg Glu Ala Leu
     315           35                  40                  45
     317 Phe Asn Ala Ile Cys Ala Tyr
     318       50                  55
     321 <210> SEQ ID NO: 7
     322 <211> LENGTH: 56
     323 <212> TYPE: PRT
     324 <213> ORGANISM: Vitreoscilla stercoraria
     326 <400> SEQUENCE: 7
     327 Ile Ile Lys Ala Thr Val Pro Val Leu Lys Glu His Gly Val Thr Ile
     328   1               5                  10                  15
     330 Thr Thr Thr Phe Tyr Lys Asn Leu Phe Ala Lys His Pro Glu Val Arg
     331               20                  25                  30
     333 Pro Leu Phe Asp Met Gly Arg Gln Glu Ser Leu Glu Gln Pro Lys Ala
     334           35                  40                  45
     336 Leu Ala Met Thr Val Leu Ala Ala
     337       50                  55
     340 <210> SEQ ID NO: 8
     341 <211> LENGTH: 55
     342 <212> TYPE: PRT
```

<2227 must contain location of all Xaa's. If Xaa's are all the same use of a range to describe the location is fine. See item #9 on Error Summary Sheet

FYI:

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 07/07/2001
PATENT APPLICATION: US/09/455,978 TIME: 13:15:01

Input Set : A:\H1020011.app
Output Set: N:\CRF3\07062001\I455978.raw

L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:1703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83
L:1744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84
L:1763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85
L:1785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86